

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Xu, Hong-Ji  
Hu, Shi-Xue  
Benedict, William F.  
Zhou, Yunli
- (ii) TITLE OF INVENTION: MODIFIED RETINOBLASTOMA TUMOR SUPPRESSOR  
PROTEINS
- (iii) NUMBER OF SEQUENCES: 51
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Arnold, White & Durkee
  - (B) STREET: P.O. Box 4433
  - (C) CITY: Houston
  - (D) STATE: TX
  - (E) COUNTRY: USA
  - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US UNKNOWN
  - (B) FILING DATE: Concurrently Herewith
  - (C) CLASSIFICATION: UNKNOWN
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/038,118
  - (B) FILING DATE: 20-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Hibler, David W.
  - (B) REGISTRATION NUMBER: 41,071
  - (C) REFERENCE/DOCKET NUMBER: UTXC:506
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 512/418-3000
  - (B) TELEFAX: 512/474-7577

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	

ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
240 245 250	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
255 260 265 270	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
275 280 285	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
290 295 300	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
305 310 315	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	1008
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
320 325 330	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	1056
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
335 340 345 350	
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	1104
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
355 360 365	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
370 375 380	

CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
385 390 395	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	1248
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
400 405 410	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	1296
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
415 420 425 430	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1344
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
435 440 445	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1392
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
450 455 460	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1440
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
465 470 475	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1488
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
480 485 490	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1536
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
495 500 505 510	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1584
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
515 520 525	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
530 535 540	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
545 550 555	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
560 565 570	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
575 580 585 590	

CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
595 600 605	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
610 615 620	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
735 740 745 750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
755 760 765	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
770 775 780	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
785 790 795	

ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys 800 805 810	2448
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg 815 820 825 830	2496
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln 835 840 845	2544
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser 850 855 860	2592
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp 865 870 875	2640
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu 880 885 890	2688
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg 895 900 905 910	2736
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu 915 920 925	2784
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTTCATTG Glu Lys	2840
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2960
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3200
TTAATTTAAC ATGAACACCC TTAGAAAAATG TGTCCATCT ATCTTCCAAA TGCAATTTGA	3260
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA	3320
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT	3380

ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT 3440  
 AACCATATGA TACTATCATA CTACTGAAAC AGATTTCATA CCTCAGAATG TAAAAGAACT 3500  
 TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGTC 3555

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala  
 1 5 10 15  
 Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp  
 20 25 30  
 Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu  
 35 40 45  
 Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu  
 50 55 60  
 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
 65 70 75 80  
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
 85 90 95  
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu  
 100 105 110  
 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val  
 115 120 125  
 His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
 130 135 140  
 Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala  
 145 150 155 160  
 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
 165 170 175  
 Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
 180 185 190

Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	195	200	205	
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	210	215	220	
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235	240
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	245	250	255	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	260	265	270	
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	275	280	285	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	290	295	300	
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315	320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395	400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430	
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475	480

Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	530	535	540
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	545	550	555
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	565	570	575
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	580	585	590
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	595	600	605
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	610	615	620
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	625	630	635
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	645	650	655
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	660	665	670
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	675	680	685
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	690	695	700
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	705	710	715
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	725	730	735
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	740	745	750
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	755	760	765

Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His
770						775					780				
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790					795					800
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
			805						810					815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
	835						840					845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
				885					890					895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
	915						920					925			

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGTC ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	48
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
1 5 10	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	96
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
15 20 25 30	

AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	144
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
35 40 45	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	192
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
50 55 60	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	240
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
65 70 75	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	288
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
80 85 90	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	336
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
95 100 105 110	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	384
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
115 120 125	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	432
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
130 135 140	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	480
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
145 150 155	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	528
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
160 165 170	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	576
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
175 180 185 190	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	624
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
195 200 205	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	672
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
210 215 220	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	720
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
225 230 235	

TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val 240 245 250	768
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile 255 260 265 270	816
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu 275 280 285	864
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser 290 295 300	912
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe 305 310 315	960
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr 320 325 330	1008
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys 335 340 345 350	1056
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn 355 360 365	1104
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val 370 375 380	1152
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr 385 390 395	1200
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe 400 405 410	1248
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu 415 420 425 430	1296
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met 435 440 445	1344

GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1392
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
450 455 460	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1440
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
465 470 475	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1488
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
480 485 490	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1536
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
495 500 505 510	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1584
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
515 520 525	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1632
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
530 535 540	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	1680
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
545 550 555	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	1728
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
560 565 570	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	1776
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
575 580 585 590	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	1824
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
595 600 605	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	1872
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
610 615 620	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	1920
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
625 630 635	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	1968
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
640 645 650	

AAT Asn	ATT Ile	TTG Leu	CAG Gln	TAT Tyr	GCT Ala	TCC Ser	ACC Thr	AGG Arg	CCC Pro	CCT Pro	ACC Thr	TTG Leu	TCA Ser	CCA Pro	ATA Ile	2016
655				660				665				670				
CCT Pro	CAC His	ATT Ile	CCT Pro	CGA Arg	AGC Ser	CCT Pro	TAC Tyr	AAG Lys	TTT Phe	CCT Pro	AGT Ser	TCA Ser	CCC Pro	TTA Leu	CGG Arg	2064
675				680				685								
ATT Ile	CCT Pro	GGA Gly	GGG Gly	AAC Asn	ATC Ile	TAT Tyr	ATT Ile	TCA Ser	CCC Pro	CTG Leu	AAG Lys	AGT Ser	CCA Pro	TAT Tyr	AAA Lys	2112
690				695				700								
ATT Ile	TCA Ser	GAA Glu	GGT Gly	CTG Leu	CCA Pro	ACA Thr	CCA Pro	ACA Thr	AAA Lys	ATG Met	ACT Thr	CCA Pro	AGA Arg	TCA Ser	AGA Arg	2160
705				710				715								
ATC Ile	TTA Leu	GTA Val	TCA Ser	ATT Ile	GGT Gly	GAA Glu	TCA Ser	TTC Phe	GGG Gly	ACT Thr	TCT Ser	GAG Glu	AAG Lys	TTC Phe	CAG Gln	2208
720				725				730								
AAA Lys	ATA Ile	AAT Asn	CAG Gln	ATG Met	GTA Val	TGT Cys	AAC Asn	AGC Ser	GAC Asp	CGT Arg	GTG Val	CTC Leu	AAA Lys	AGA Arg	AGT Ser	2256
735				740				745				750				
GCT Ala	GAA Glu	GGA Gly	AGC Ser	AAC Asn	CCT Pro	CCT Pro	AAA Lys	CCA Pro	CTG Leu	AAA Lys	AAA Lys	CTA Leu	CGC Arg	TTT Phe	GAT Asp	2304
755				760				765								
ATT Ile	GAA Glu	GGA Gly	TCA Ser	GAT Asp	GAA Glu	GCA Ala	GAT Asp	GGA Gly	AGT Ser	AAA Lys	CAT His	CTC Leu	CCA Pro	GGA Gly	GAG Glu	2352
770				775				780								
TCC Ser	AAA Lys	TTT Phe	CAG Gln	CAG Gln	AAA Lys	CTG Leu	GCA Ala	GAA Glu	ATG Met	ACT Thr	TCT Ser	ACT Thr	CGA Arg	ACA Thr	CGA Arg	2400
785				790				795								
ATG Met	CAA Gln	AAG Lys	CAG Gln	AAA Lys	ATG Met	AAT Asn	GAT Asp	AGC Ser	ATG Met	GAT Asp	ACC Thr	TCA Ser	AAC Asn	AAG Lys	GAA Glu	2448
800				805				810								
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG																2504
Glu Lys																
815																
TCTCTCACAG ATGTGACTGT ATAAC TTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC																2564
TTCAGCTCTT TTTGTGGATA TAA AATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC																2624
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTG TGTA AATCCTGCCA																2684
TTTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT																2744
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT																2804

TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT 2864  
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCCTATCT ATCTTCCAAA TGCAATTTGA 2924  
TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA 2984  
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT 3044  
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT 3104  
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT 3164  
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT 3218

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val  
1 5 10 15  
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
20 25 30  
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala  
35 40 45  
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
50 55 60  
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
65 70 75 80  
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met  
85 90 95  
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp  
100 105 110  
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys  
115 120 125  
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly  
130 135 140

Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	145	150	155	160
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	165	170	175	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	180	185	190	
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	195	200	205	
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	210	215	220	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	225	230	235	240
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	245	250	255	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	260	265	270	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	275	280	285	
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	290	295	300	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	305	310	315	320
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	325	330	335	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	340	345	350	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	355	360	365	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	370	375	380	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	385	390	395	400
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	405	410	415	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	420	425	430	

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser	435	440	445
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser	450	455	460
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu	465	470	475 480
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser	485	490	495
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser	500	505	510
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys	515	520	525
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg	530	535	540
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu	545	550	555 560
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu	565	570	575
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met	580	585	590
Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys	595	600	605
Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln	610	615	620
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile	625	630	635 640
Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile	645	650	655
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His	660	665	670
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro	675	680	685
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser	690	695	700
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu	705	710	715 720

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile  
725 730 735

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu  
740 745 750

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu  
755 760 765

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys  
770 775 780

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln  
785 790 795 800

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
805 810 815

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCGAGCAAT GGGCGTGATA GCGGTTTGAC TCACGGGGAT TTCCAAGTCT CCACCCCATT	60
GACGTCAATG GGAGTTTGTT TTGGCACCAA AATCAACGGG ACTTTCCAAA ATGTCGTAAC	120
AACTCCGCCC CATTGACGCA AATGGGCGGT AGGCGTGTAC GGTGGGAGGT CTATATAAGC	180
AGAGCTCGTT TAGTGAACCG TCAGATCGCC TGGAGACGCC ATCCACGCTG TTTTGACCTC	240
CATAGAAGAC ACCGGGACCG ATCCAGCCTC CGCGGCCGCG AATTC	285

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTCGAGC AATGGGCGTG GATAGCGG	28
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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGCTCGAGC ACCAAAATCA ACGGGA

26

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGCTCGAGC AACTCCGCCC CATTGAC

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGACATATG AATTCGCGGC C

21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGAATTCTG CTGTCTGCG

19

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCTCTAGATG CAGTTGGACC TGGGAG

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTG CCGCCATGTC GTTCACTTTT AC

32

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCCAAGAGA ATTCATAAAA GG

22

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCAAGCTTG CCGCCATGGA GCAGGACAGC GGCCCCGGAC

39

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCAAGCTTG CCGCCATGGA TTTTACTGCA TTATGTCAG

39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCCAAGCTTG CCGCCATGGA GAAAGTTTCA TCTTGTGAT

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAAGCTTG CCGCCATGCT GTGGGGAATC TGTATCTTT

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCAAGCTTG CCGCCATGTC AAGACTGTTG AAGAAG

36

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
GCGCCTGAGG ACCTAGATGA GATGTCGTTC 30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
GCGGTTAACC CTAGATGAGA TGTCGTTTAC T 31

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
CCCAAGCTTG CCGTCATGCC GCCCAAACC CCCC GA 36

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
CTCACCTAGG TCAACTGCTG CAAT 24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTTGACCTAG GTGATATGTC GTTC

24

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCGCCTAGGA TCTACTGAAA TAAATTCTGC A

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCGATATCA ACTGCTGGGT TGTGTCAAAT A

31

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCCGAATTCG TTTTATATGG TTCTTTGAGC AA

32

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 4..5

(D) OTHER INFORMATION: /note= "R=A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCRCCAUGG

10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..2691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCCGTC ATG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG CTT	48
Met Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu	
1 5 10	
GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG AAA	96
Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys	
15 20 25 30	
TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG	144
Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu	
35 40 45	
AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA	192
Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys	
50 55 60	
AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT	240
Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp	
65 70 75	
GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT	288
Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser	
80 85 90	
GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA	336
Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys	
95 100 105 110	
GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT	384
Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe	
115 120 125	

GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA	432
Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr	
130 135 140	
CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA	480
Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu	
145 150 155	
AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA	528
Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln	
160 165 170	
ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT	576
Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu	
175 180 185 190	
GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT	624
Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr	
195 200 205	
AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA	672
Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg	
210 215 220	
GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA	720
Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr	
225 230 235	
AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG	768
Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu	
240 245 250	
GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT	816
Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu	
255 260 265 270	
GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA	864
Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys	
275 280 285	
CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA	912
Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu	
290 295 300	
TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT	960
Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe	
305 310 315	
GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT	1008
Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn	
320 325 330	

GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA	1056
Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln	
335 340 345 350	
CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT	1104
Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn	
355 360 365	
CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA	1152
Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile	
370 375 380	
CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT	1200
Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala	
385 390 395	
AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA	1248
Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys	
400 405 410	
CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA	1296
Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser	
415 420 425 430	
GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC	1344
Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp	
435 440 445	
AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG	1392
Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met	
450 455 460	
GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT	1440
Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp	
465 470 475	
TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT	1488
Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp	
480 485 490	
TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA	1536
Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr	
495 500 505 510	
AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA	1584
Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu	
515 520 525	
TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA	1632
Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln	
530 535 540	

TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT	1680
Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro	
545 550 555	
CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT	1728
Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu	
560 565 570	
TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT	1776
Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn	
575 580 585 590	
TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG	1824
Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln	
595 600 605	
AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT	1872
Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr	
610 615 620	
CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT	1920
Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser	
625 630 635	
GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC	1968
Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr	
640 645 650	
CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT	2016
Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile	
655 660 665 670	
ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT	2064
Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu	
675 680 685	
AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT	2112
Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val	
690 695 700	
CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT	2160
Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser	
705 710 715	
ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT	2208
Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn	
720 725 730	
ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT	2256
Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro	
735 740 745 750	

CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT	2304
His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile	
755 760 765	
CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT	2352
Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile	
770 775 780	
TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC	2400
Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile	
785 790 795	
TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA	2448
Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys	
800 805 810	
ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT	2496
Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala	
815 820 825 830	
GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT	2544
Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile	
835 840 845	
GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC	2592
Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser	
850 855 860	
AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG	2640
Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met	
865 870 875	
CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG	2688
Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu	
880 885 890	
AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2741
Lys	
895	
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2801
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2861
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	2921
TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	2981
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3041
TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT	3101
TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA	3161

TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA 3221  
ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT 3281  
ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT 3341  
AACCATATGA TACTATCATA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT 3401  
TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT 3455

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu Phe  
1 5 10 15  
Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu Lys  
20 25 30  
Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys Val  
35 40 45  
Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys Glu  
50 55 60  
Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu Met  
65 70 75 80  
Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val His  
85 90 95  
Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val Asp  
100 105 110  
Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu  
115 120 125  
Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro  
130 135 140  
Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val  
145 150 155 160  
Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu  
165 170 175

Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	180	185	190
Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	195	200	205
Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	210	215	220
Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	225	230	235
Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	245	250	255
Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	260	265	270
Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	275	280	285
Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	290	295	300
Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	305	310	315
Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	325	330	335
Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	340	345	350
Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	355	360	365
Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	370	375	380
Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	385	390	395
Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	405	410	415
Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	420	425	430
Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	435	440	445
Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	450	455	460

Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	465	470	475	480
Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	485	490	495	
Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	500	505	510	
Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	515	520	525	
Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	530	535	540	
Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	545	550	555	560
Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	565	570	575	
Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	580	585	590	
Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	595	600	605	
Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	610	615	620	
Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	625	630	635	640
Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	645	650	655	
Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	660	665	670	
Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	675	680	685	
Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	690	695	700	
Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	705	710	715	720
Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	725	730	735	
Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	740	745	750	

Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly  
 755 760 765  
 Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu  
 770 775 780  
 Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val  
 785 790 795 800  
 Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn  
 805 810 815  
 Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly  
 820 825 830  
 Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly  
 835 840 845  
 Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe  
 850 855 860  
 Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys  
 865 870 875 880  
 Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
 885 890 895

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3392 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCATC ATG GAT TTT ACT GCA TTA TGT CAG AAA TTA AAG ATA CCA GAT	48
Met Asp Phe Thr Ala Leu Cys Gln Lys Leu Lys Ile Pro Asp	
1 5 10	
CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG GAG AAA GTT TCA TCT GTG	96
His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys Val Ser Ser Val	
15 20 25 30	
GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG AAA AAG GAA CTG TGG GGA	144
Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys Glu Leu Trp Gly	
35 40 45	

ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA GAT GAG ATG TCG TTC ACT	192
Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu Met Ser Phe Thr	
50 55 60	
TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC AGT GTC CAT AAA TTC TTT	240
Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val His Lys Phe Phe	
65 70 75	
AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC AAA GTT GAT AAT GCT ATG	288
Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val Asp Asn Ala Met	
80 85 90	
TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC TTC AGC AAA	336
Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu Phe Ser Lys	
95 100 105 110	
TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC AGC AGT TCG	384
Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro Ser Ser Ser	
115 120 125	
ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG ATC	432
Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp Ile	
130 135 140	
ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT CTG	480
Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp Leu	
145 150 155	
GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT AAA	528
Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile Lys	
160 165 170	
CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT ATA	576
Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val Ile	
175 180 185 190	
CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT	624
Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser	
195 200 205	
GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT	672
Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val	
210 215 220	
CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT	720
Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr	
225 230 235	
TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT	768
Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser	
240 245 250	

AAT Asn 255	GGA Gly	CTT Leu	CCA Pro	GAG Glu	GTT Val 260	GAA Glu	AAT Asn	CTT Leu	TCT Ser	AAA Lys 265	CGA Arg	TAC Tyr	GAA Glu	GAA Glu	ATT Ile 270	816
TAT Tyr	CTT Leu	AAA Lys	AAT Asn	AAA Lys 275	GAT Asp	CTA Leu	GAT Asp	GCA Ala	AGA Arg	TTA Leu	TTT Phe	TTG Leu	GAT Asp	CAT His	GAT Asp 285	864
AAA Lys	ACT Thr	CTT Leu	CAG Gln 290	ACT Thr	GAT Asp	TCT Ser	ATA Ile	GAC Asp	AGT Ser	TTT Phe	GAA Glu	ACA Thr	CAG Gln	AGA Arg	ACA Thr	912
CCA Pro	CGA Arg	AAA Lys 305	AGT Ser	AAC Asn	CTT Leu	GAT Asp	GAA Glu 310	GAG Glu	GTG Val	AAT Asn	GTA Val	ATT Ile 315	CCT Pro	CCA Pro	CAC His	960
ACT Thr 320	CCA Pro	GTT Val	AGG Arg	ACT Thr	GTT Val	ATG Met 325	AAC Asn	ACT Thr	ATC Ile	CAA Gln 330	CAA Gln	TTA Leu	ATG Met	ATG Met	ATT Ile	1008
TTA Leu 335	AAT Asn	TCA Ser	GCA Ala	AGT Ser	GAT Asp 340	CAA Gln	CCT Pro	TCA Ser	GAA Glu	AAT Asn 345	CTG Leu	ATT Ile	TCC Ser	TAT Tyr	TTT Phe 350	1056
AAC Asn	AAC Asn	TGC Cys	ACA Thr	GTG Val 355	AAT Asn	CCA Pro	AAA Lys	GAA Glu 360	AGT Ser	ATA Ile	CTG Leu	AAA Lys	AGA Arg	GTG Val 365	AAG Lys	1104
GAT Asp	ATA Ile	GGA Gly	TAC Tyr 370	ATC Ile	TTT Phe	AAA Lys	GAG Glu	AAA Lys 375	TTT Phe	GCT Ala	AAA Lys	GCT Ala	GTG Val 380	GGA Gly	CAG Gln	1152
GGT Gly	TGT Cys	GTC Val 385	GAA Glu	ATT Ile	GGA Gly	TCA Ser	CAG Gln 390	CGA Arg	TAC Tyr	AAA Lys	CTT Leu	GGA Gly 395	GTT Val	CGC Arg	TTG Leu	1200
TAT Tyr 400	TAC Tyr	CGA Arg	GTA Val	ATG Met	GAA Glu	TCC Ser	ATG Met 405	CTT Leu	AAA Lys	TCA Ser	GAA Glu 410	GAA Glu	GAA Glu	CGA Arg	TTA Leu	1248
TCC Ser 415	ATT Ile	CAA Gln	AAT Asn	TTT Phe	AGC Ser	AAA Lys	CTT Leu	CTG Leu	AAT Asn	GAC Asp 425	AAC Asn	ATT Ile	TTT Phe	CAT His	ATG Met 430	1296
TCT Ser	TTA Leu	TTG Leu	GCG Ala	TGC Cys 435	GCT Ala	CTT Leu	GAG Glu	GTT Val	GTA Val 440	ATG Met	GCC Ala	ACA Thr	TAT Tyr	AGC Ser	AGA Arg 445	1344
AGT Ser	ACA Thr	TCT Ser	CAG Gln 450	AAT Asn	CTT Leu	GAT Asp	TCT Ser	GGA Gly 455	ACA Thr	GAT Asp	TTG Leu	TCT Ser	TTC Phe	CCA Pro	TGG Trp	1392

ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC	1440
Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile	
465 470 475	
GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA	1488
Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys	
480 485 490	
CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC	1536
His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu	
495 500 505 510	
TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA	1584
Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu	
515 520 525	
GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC	1632
Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu	
530 535 540	
CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT	1680
Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser	
545 550 555	
CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA	1728
Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala	
560 565 570	
GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT	1776
Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser	
575 580 585 590	
ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC	1824
Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu	
595 600 605	
CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA	1872
Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu	
610 615 620	
GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT	1920
Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr	
625 630 635	
GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG	1968
Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met	
640 645 650	
TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT	2016
Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile	
655 660 665 670	

GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA	2064
Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys	
675 680 685	
CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT	2112
Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr	
690 695 700	
AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT	2160
Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala	
705 710 715	
TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC	2208
Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser	
720 725 730	
CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC	2256
Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile	
735 740 745 750	
TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA	2304
Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro	
755 760 765	
ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT	2352
Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly	
770 775 780	
GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA	2400
Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val	
785 790 795	
TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT	2448
Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro	
800 805 810	
CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA	2496
Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu	
815 820 825 830	
GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA	2544
Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys	
835 840 845	
CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG	2592
Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met	
850 855 860	
AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC	2638
Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
865 870	
AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT	2698

ATAACTTTCC CAGGTTCTGT TTATG3CCAC ATTTAATATC TTCAGCTCTT TTTGTGGATA	2758
TAAAATGTGC AGATGCAATT GTTTG3GTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG	2818
TTATTTATAC AAGATTGAAA ATCTT3TGTA AATCCTGCCA TTTAAAAAGT TGTAGCAGAT	2878
TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT	2938
GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG	2998
ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC ATGAACACCC	3058
TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC ATTCACCAAA	3118
ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT	3178
TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA	3238
AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA	3298
CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC	3358
CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3392

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val
1				5					10					15	
Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly
			20					25					30		
Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys
		35					40					45			
Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr
	50					55					60				
Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu
65				70					75					80	
Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg
			85					90						95	

Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	100	105	110	
Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	115	120	125	
Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	130	135	140	
Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	145	150	155	160
Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	165	170	175	
Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	180	185	190	
Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	195	200	205	
Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	210	215	220	
Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	225	230	235	240
Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	245	250	255	
Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	260	265	270	
Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	275	280	285	
Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	290	295	300	
Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	305	310	315	320
Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	325	330	335	
Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	340	345	350	
Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	355	360	365	
Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	370	375	380	

Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	385	390	395	400
Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	405	410	415	
Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	420	425	430	
Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	435	440	445	
Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	450	455	460	
Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	465	470	475	480
Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	485	490	495	
Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	500	505	510	
Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	515	520	525	
Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	530	535	540	
Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	545	550	555	560
Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	565	570	575	
Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	580	585	590	
Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	595	600	605	
Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	610	615	620	
Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	625	630	635	640
Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	645	650	655	
Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	660	665	670	

Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val		
675	680	685
Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser		
690	695	700
Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr		
705	710	715 720
Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr		
	725	730 735
Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile		
	740	745 750
Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro		
	755	760 765
Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser		
	770	775 780
Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn		
785	790	795 800
Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys		
	805	810 815
Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp		
	820	825 830
Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala		
	835	840 845
Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp		
	850	855 860
Ser Met Asp Thr Ser Asn Lys Glu Glu Lys		
865	870	

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCCATC ATG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT	48
Met Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
1 5 10	
ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA	96
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
15 20 25 30	
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
115 120 125	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	432
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
130 135 140	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	480
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
145 150 155	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	528
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160 165 170	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	576
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
175 180 185 190	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	624
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
195 200 205	

AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe 210 215 220	672
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu 225 230 235	720
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu 240 245 250	768
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser 255 260 265 270	816
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp 275 280 285	864
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met 290 295 300	912
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln 305 310 315	960
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro 320 325 330	1008
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys 335 340 345 350	1056
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser 355 360 365	1104
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser 370 375 380	1152
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys 385 390 395	1200
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu 400 405 410	1248

GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1296
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
415 420 425 430	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1344
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
435 440 445	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1392
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
450 455 460	
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1440
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
465 470 475	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1488
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
480 485 490	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1536
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
495 500 505 510	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1584
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
515 520 525	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1632
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
530 535 540	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	1680
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
545 550 555	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	1728
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
560 565 570	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	1776
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
575 580 585 590	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	1824
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
595 600 605	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	1872
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
610 615 620	

TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	1920
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
625 630 635	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	1968
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
640 645 650	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2016
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
655 660 665 670	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2064
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg	
675 680 685	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG	2112
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu	
690 695 700	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA	2160
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser	
705 710 715	
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT	2208
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser	
720 725 730	
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA	2256
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro	
735 740 745 750	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG	2304
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu	
755 760 765	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2352
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
770 775 780	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2400
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
785 790 795	
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2448
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
800 805 810	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2496
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
815 820 825 830	

CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2544
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
835 840 845	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2599
Asn Lys Glu Glu Lys	
850	
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT TTATGGCCAC	2659
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2779
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGCCTATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3139
AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG	3259
TAAAAGAAGT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA	3319
TAGT	3323

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln	
1 5 10 15	
Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp	
20 25 30	
Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu	
35 40 45	

Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser  
50 55 60

Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val  
65 70 75 80

Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr  
85 90 95

Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu  
100 105 110

Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val  
115 120 125

Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys  
130 135 140

Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu  
145 150 155 160

Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro  
165 170 175

Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn  
180 185 190

Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile  
195 200 205

Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn  
210 215 220

Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu  
225 230 235 240

Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala  
245 250 255

Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp  
260 265 270

Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu  
275 280 285

Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr  
290 295 300

Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser  
305 310 315 320

Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu  
325 330 335

Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys		
			340					345					350				
Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg		
		355					360					365					
Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu		
	370					375					380						
Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu		
385					390					395					400		
Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val		
			405						410					415			
Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly		
		420						425					430				
Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala		
	435						440					445					
Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn		
	450					455					460						
Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile		
465					470				475					480			
Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile		
			485					490					495				
Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala		
		500						505					510				
Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met		
		515					520					525					
Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg		
	530					535					540						
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln		
545					550				555					560			
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys		
			565					570					575				
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu		
			580					585					590				
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln		
	595						600					605					
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp		
	610					615					620						

Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	625	630	635	640
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	645	650	655	
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	660	665	670	
Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	675	680	685	
Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	690	695	700	
Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	705	710	715	720
Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	725	730	735	
Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	740	745	750	
Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	755	760	765	
Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	770	775	780	
Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	785	790	795	800
Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	805	810	815	
Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	820	825	830	
Arg	Met	Gln	Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	835	840	845	
Glu	Glu	Lys														850			

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..2502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCATC ATG CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	48
Met Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
1 5 10	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	96
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
15 20 25 30	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	144
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
35 40 45	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	192
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
50 55 60	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	240
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
65 70 75	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	288
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
80 85 90	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	336
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
95 100 105 110	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	384
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
115 120 125	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	432
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
130 135 140	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	480
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
145 150 155	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	528
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
160 165 170	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	576
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
175 180 185 190	

GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser 195 200 205	624
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser 210 215 220	672
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg 225 230 235	720
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser 240 245 250	768
TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val 255 260 265 270	816
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile 275 280 285	864
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu 290 295 300	912
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser 305 310 315	960
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe 320 325 330	1008
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr 335 340 345 350	1056
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys 355 360 365	1104
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn 370 375 380	1152
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val 385 390 395	1200

ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1248
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
400 405 410	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1296
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
415 420 425 430	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1344
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
435 440 445	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1392
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
450 455 460	
GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1440
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
465 470 475	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1488
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
480 485 490	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1536
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
495 500 505 510	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1584
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
515 520 525	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1632
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
530 535 540	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1680
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
545 550 555	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	1728
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
560 565 570	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	1776
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
575 580 585 590	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	1824
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
595 600 605	

ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	1872
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
610 615 620	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	1920
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
625 630 635	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	1968
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
640 645 650	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2016
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
655 660 665 670	
AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2064
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
675 680 685	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2112
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
690 695 700	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2160
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
705 710 715	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2208
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
720 725 730	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG	2256
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln	
735 740 745 750	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT	2304
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser	
755 760 765	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2352
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
770 775 780	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG	2400
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu	
785 790 795	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2448
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg	
800 805 810	



Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	50	55	60	
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	65	70	75	80
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	85	90	95	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	100	105	110	
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	115	120	125	
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	130	135	140	
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	145	150	155	160
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	165	170	175	
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	180	185	190	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	195	200	205	
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	210	215	220	
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	225	230	235	240
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	245	250	255	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	260	265	270	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	275	280	285	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	290	295	300	
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	305	310	315	320
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	325	330	335	

Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	340	345	350	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	355	360	365	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	370	375	380	
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	385	390	395	400
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	405	410	415	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	420	425	430	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	435	440	445	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	450	455	460	
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	465	470	475	480
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	485	490	495	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	500	505	510	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	515	520	525	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	530	535	540	
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	545	550	555	560
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	565	570	575	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	580	585	590	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	595	600	605	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	610	615	620	

Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	625	630	635	640
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	645	650	655	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	660	665	670	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	675	680	685	
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	690	695	700	
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	705	710	715	720
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	725	730	735	
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	740	745	750	
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	755	760	765	
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	770	775	780	
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	785	790	795	800
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	805	810	815	
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys	820	825	830	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCCGTC ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG TTT GCA CTC	48
Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala Leu	
1 5 10	
TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG ACA CAA CCC	96
Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln Pro	
15 20 25 30	
AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT	144
Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val	
35 40 45	
TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA	192
Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu	
50 55 60	
GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT	240
Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr	
65 70 75	
TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA	288
Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr	
80 85 90	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	336
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
95 100 105 110	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	384
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
115 120 125	
ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA	432
Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys	
130 135 140	
AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT	480
Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu	
145 150 155	
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC	528
Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr	
160 165 170	
GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG	576
Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu	
175 180 185 190	
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA	624
Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr	
195 200 205	

CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT	672
Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile	
210 215 220	
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA	720
Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu	
225 230 235	
ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT	768
Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile	
240 245 250	
TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA	816
Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys	
255 260 265 270	
AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT	864
Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala	
275 280 285	
GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA	912
Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly	
290 295 300	
GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA	960
Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu	
305 310 315	
GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT	1008
Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile	
320 325 330	
TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA	1056
Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr	
335 340 345 350	
TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT	1104
Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser	
355 360 365	
TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC	1152
Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr	
370 375 380	
AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA	1200
Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu	
385 390 395	
ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT	1248
Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu	
400 405 410	

GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG	1296
Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys	
415 420 425 430	
GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT	1344
Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn	
435 440 445	
CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT	1392
Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro	
450 455 460	
GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT	1440
Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr	
465 470 475	
GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA	1488
Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro	
480 485 490	
TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA	1536
Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu	
495 500 505 510	
GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC	1584
Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His	
515 520 525	
CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG	1632
Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln	
530 535 540	
AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG	1680
Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met	
545 550 555	
TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC	1728
Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe	
560 565 570	
AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG	1776
Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu	
575 580 585 590	
ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA	1824
Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile	
595 600 605	
GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1872
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
610 615 620	

CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile 625 630 635	1920
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly 640 645 650	1968
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu 655 660 665 670	2016
GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val 675 680 685	2064
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn 690 695 700	2112
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly 705 710 715	2160
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly 720 725 730	2208
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe 735 740 745 750	2256
CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys 755 760 765	2304
CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys 770 775 780	2349
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2409
ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2469
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2529
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2589
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2649
GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG	2709
CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC	2769

ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC	2829
ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA	2889
AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT ACTGTGTGCT	2949
TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA	3009
TACTATCATA CTACTGAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT	3069
TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3113

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	Leu	Phe	Ser	1	5	10	15
Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	Pro	Ser	Ser	20	25	30	
Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	Val	Ser	Trp	35	40	45	
Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	Glu	Asp	Asp	50	55	60	
Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	Tyr	Phe	Ile	65	70	75	80
Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	Thr	Ala	Val	85	90	95	
Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	Gln	Asn	Arg	100	105	110	
Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	Ile	Ile	Glu	115	120	125	
Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	Lys	Asn	Val	130	135	140	
Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	Leu	Val	Thr	145	150	155	160

Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	
				165					170					175		
Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	
			180					185					190			
Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	Thr	Gln	Arg	
		195					200					205				
Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	Ile	Pro	Pro	
	210					215					220					
His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	Leu	Met	Met	
225					230					235					240	
Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	
			245						250					255		
Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	
			260					265					270			
Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	
	275						280					285				
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	
	290					295					300					
Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	
305					310					315					320	
Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	
			325						330					335		
Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	
		340						345					350			
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	
		355					360					365				
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	
	370					375					380					
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	
385					390					395					400	
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	
			405						410					415		
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	
		420						425					430			
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	
	435						440						445			

Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	450	455	460	
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	465	470	475	480
Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	485	490	495	
Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	500	505	510	
Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	515	520	525	
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	530	535	540	
Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	545	550	555	560
Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	565	570	575	
Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	580	585	590	
Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	595	600	605	
Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	610	615	620	
Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	625	630	635	640
Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	645	650	655	
Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	660	665	670	
Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	675	680	685	
Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	690	695	700	
Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	705	710	715	720
Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	725	730	735	

Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln  
740 745 750

Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys  
755 760 765

Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
770 775 780

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GTC GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC	144
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
35 40 45	
ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT	192
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
50 55 60	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT	240
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
65 70 75	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT	288
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	
80 85 90	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT	336
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
95 100 105 110	

GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG	384
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	
115 120 125	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG	432
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	
130 135 140	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC	480
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	
145 150 155	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA	528
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	
160 165 170	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA	576
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	
175 180 185 190	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT	624
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	
195 200 205	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT	672
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	
210 215 220	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA	720
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	
225 230 235	
AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA	768
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	
240 245 250	
GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	816
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser	
255 260 265 270	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	864
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp	
275 280 285	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	912
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met	
290 295 300	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	960
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln	
305 310 315	

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1008
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro	
320 325 330	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1056
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys	
335 340 345 350	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1104
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser	
355 360 365	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1152
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser	
370 375 380	
ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1200
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys	
385 390 395	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1248
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu	
400 405 410	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1296
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp	
415 420 425 430	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1344
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu	
435 440 445	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1392
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu	
450 455 460	
GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1440
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
465 470 475	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1488
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
480 485 490	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1536
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
495 500 505 510	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1584
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
515 520 525	

GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1632
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
530 535 540	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	1680
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
545 550 555	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	1728
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
560 565 570	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	1776
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
575 580 585 590	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	1824
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
595 600 605	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	1872
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
610 615 620	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	1920
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
625 630 635	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	1968
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
640 645 650	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2016
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
655 660 665 670	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2064
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg	
675 680 685	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG	2112
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu	
690 695 700	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA	2160
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser	
705 710 715	
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT	2208
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser	
720 725 730	

CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA	2256
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro	
735 740 745 750	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG	2304
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu	
755 760 765	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC	2352
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu	
770 775 780	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA	2400
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu	
785 790 795	
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC	2448
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu	
800 805 810	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT	2496
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr	
815 820 825 830	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA	2544
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser	
835 840 845	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT	2599
Asn Lys Glu Lys	
850	
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC	2659
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAATGTGC AGATGCAATT GTTTGGGTGA	2719
TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2779
AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG	2839
CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC	2899
TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT	2959
GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA	3019
TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT	3079
ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG	3139
AATCTGATAT ACTGTGTGCT TGTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA	3199
AGCAAAGTAT AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG	3259

TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA 3319  
TAGT 3323

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Val	Asp	20	25	30	
Leu	Asp	Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	35	40	45	
Ile	Ser	Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	50	55	60	
Thr	Lys	Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	65	70	75	80
Leu	Phe	Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	85	90	95	
Leu	Thr	Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	100	105	110	
Val	Leu	Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	115	120	125	
Leu	Gln	Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	130	135	140	
Val	Leu	Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	145	150	155	160
Pro	Tyr	Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	165	170	175	
Arg	Arg	Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	180	185	190	
Asp	Thr	Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	195	200	205	

Asp	Glu	Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	210	215	220	
Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	225	230	235	240
Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	245	250	255	
Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	260	265	270	
Ser	Phe	Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	275	280	285	
Val	Asn	Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	290	295	300	
Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	305	310	315	320
Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	325	330	335	
Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	340	345	350	
Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	355	360	365	
Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	370	375	380	
Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	385	390	395	400
Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	405	410	415	
Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	420	425	430	
Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	435	440	445	
Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	450	455	460	
Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	465	470	475	480
Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	485	490	495	

Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	500	505	510	
Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	515	520	525	
Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	530	535	540	
Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	545	550	555	560
Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	565	570	575	
Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	580	585	590	
Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	595	600	605	
His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	610	615	620	
Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	625	630	635	640
Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	645	650	655	
Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	660	665	670	
Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	675	680	685	
Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	690	695	700	
Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	705	710	715	720
Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	725	730	735	
Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	740	745	750	
Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	755	760	765	
Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	770	775	780	

Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe  
785 790 795 800

Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly  
805 810 815

Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr  
820 825 830

Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys  
835 840 845

Glu Glu Lys  
850

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTG GTC GAC	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Val Asp	
65 70 75	
CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA	288
Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu	
80 85 90	

ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT	336
Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser	
95 100 105 110	
ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA	384
Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val	
115 120 125	
TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT	432
Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr	
130 135 140	
TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG	480
Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu	
145 150 155	
GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA	528
Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val	
160 165 170	
TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT	576
Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys	
175 180 185 190	
GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA	624
Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu	
195 200 205	
CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC	672
Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro	
210 215 220	
AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT	720
Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn	
225 230 235	
GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA	768
Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile	
240 245 250	
GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT	816
Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn	
255 260 265 270	
TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT	864
Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu	
275 280 285	
TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA	912
Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala	
290 295 300	

AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC	960
Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp	
305 310 315	
AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG	1008
Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu	
320 325 330	
GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT	1056
Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr	
335 340 345 350	
ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA	1104
Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser	
355 360 365	
GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA	1152
Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu	
370 375 380	
AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA	1200
Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys	
385 390 395	
TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA	1248
Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg	
400 405 410	
TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT	1296
Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu	
415 420 425 430	
AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG	1344
Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu	
435 440 445	
AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT	1392
Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val	
450 455 460	
GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA	1440
Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly	
465 470 475	
ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC	1488
Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala	
480 485 490	
TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC	1536
Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn	
495 500 505 510	

TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC	1584
Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile	
515 520 525	
ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT	1632
Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile	
530 535 540	
AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT	1680
Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala	
545 550 555	
TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG	1728
Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met	
560 565 570	
TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT	1776
Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg	
575 580 585 590	
GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG	1824
Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln	
595 600 605	
ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA	1872
Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys	
610 615 620	
GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT	1920
Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu	
625 630 635	
CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG	1968
Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln	
640 645 650	
CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC	2016
His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp	
655 660 665 670	
CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA	2064
Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile	
675 680 685	
GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT	2112
Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His	
690 695 700	
GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT	2160
Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr	
705 710 715	

GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys 720 725 730	2208
ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro 735 740 745 750	2256
ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu 755 760 765	2304
CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr 770 775 780	2352
AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser 785 790 795	2400
AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe 800 805 810	2448
CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg 815 820 825 830	2496
AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe 835 840 845	2544
GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly 850 855 860	2592
GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr 865 870 875	2640
CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys 880 885 890	2688
GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT Glu Glu Lys 895	2737
GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACCTTTCC CAGGTTCTGT TTATGGCCAC	2797
ATTTAATATC TTCAGCTCTT TTTGTGGATA TAAATGTGC AGATGCAATT GTTTGGGTGA	2857
TTCTTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA	2917

AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG 2977  
 CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC 3037  
 TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT 3097  
 GTATATTTTT TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTATCT ATCTTCCAAA 3157  
 TGCAATTTGA TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT 3217  
 ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG 3277  
 AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA 3337  
 AGCAAAGTAT AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGATG 3397  
 TAAAGAAGT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA 3457  
 TAGT 3461

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala	1	5	10	15
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp	20	25	30	
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu	35	40	45	
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu	50	55	60	
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Val	Asp	Leu	Asp	65	70	75	80
Glu	Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	85	90	95	
Val	His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	100	105	110	

Val	Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	115	120	125
Ala	Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	130	135	140
Gln	Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	145	150	155
Lys	Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	165	170	175
Met	Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	180	185	190
Asp	Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	195	200	205
Lys	Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	210	215	220
Gly	Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	225	230	235
Arg	Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	245	250	255
Val	Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	260	265	270
Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	275	280	285
Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	290	295	300
Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	305	310	315
Glu	Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	325	330	335
Val	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	340	345	350
Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	355	360	365
Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	370	375	380
Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	385	390	395

Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	405	410	415	
Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	420	425	430	
Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	435	440	445	
Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	450	455	460	
Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	465	470	475	480
Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	485	490	495	
Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	500	505	510	
Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	515	520	525	
Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	530	535	540	
Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	545	550	555	560
Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	565	570	575	
Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	580	585	590	
Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	595	600	605	
Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	610	615	620	
Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	625	630	635	640
Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	645	650	655	
Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	660	665	670	
Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	675	680	685	

Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val  
 690 695 700  
 Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser  
 705 710 715 720  
 Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn  
 725 730 735  
 Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro  
 740 745 750  
 His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile  
 755 760 765  
 Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile  
 770 775 780  
 Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile  
 785 790 795 800  
 Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys  
 805 810 815  
 Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala  
 820 825 830  
 Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile  
 835 840 845  
 Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser  
 850 855 860  
 Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met  
 865 870 875 880  
 Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu  
 885 890 895  
 Lys

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GTC GAA TCT ACT GAA ATA AAT TCT GCA TTG GTG CTA AAA GTT TCT TGG	384
Val Glu Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp	
115 120 125	
ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA CAA ATG GAA GAT GAT	432
Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp	
130 135 140	
CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC CTT GAC TAT TTT ATT	480
Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile	
145 150 155	
AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA TAT AAA ACA GCT GTT	528
Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val	
160 165 170	
ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG	576
Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg	
175 180 185 190	

AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA	624
Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu	
195 200 205	
GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT	672
Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val	
210 215 220	
TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA	720
Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr	
225 230 235	
TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA	768
Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu	
240 245 250	
ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT	816
Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His	
255 260 265 270	
GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA	864
Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg	
275 280 285	
ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA	912
Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro	
290 295 300	
CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG	960
His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met	
305 310 315	
ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT	1008
Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr	
320 325 330	
TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG	1056
Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val	
335 340 345 350	
AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA	1104
Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly	
355 360 365	
CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC	1152
Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg	
370 375 380	
TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA	1200
Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg	
385 390 395	

TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT	1248
Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His	
400 405 410	
ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC	1296
Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser	
415 420 425 430	
AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA	1344
Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro	
435 440 445	
TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG	1392
Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val	
450 455 460	
ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA	1440
Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile	
465 470 475	
AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG	1488
Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp	
480 485 490	
CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA	1536
Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg	
495 500 505 510	
GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT	1584
Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro	
515 520 525	
CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA	1632
Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg	
530 535 540	
TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT	1680
Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn	
545 550 555	
GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA	1728
Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys	
560 565 570	
TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT	1776
Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr	
575 580 585 590	
CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA	1824
Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu	
595 600 605	

TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu 610 615 620	1872
TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser 625 630 635	1920
ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile 640 645 650	1968
ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe 655 660 665 670	2016
AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe 675 680 685	2064
TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr 690 695 700	2112
GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg 705 710 715	2160
AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn 720 725 730	2208
ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu 735 740 745 750	2256
CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile 755 760 765	2304
GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met 770 775 780	2352
GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn 785 790 795	2400
CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp 800 805 810	2448



Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp  
 20 25 30  
 Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu  
 35 40 45  
 Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu  
 50 55 60  
 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
 65 70 75 80  
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
 85 90 95  
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Val Glu  
 100 105 110  
 Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys Val Ser Trp Ile Thr  
 115 120 125  
 Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met Glu Asp Asp Leu Val  
 130 135 140  
 Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu  
 145 150 155 160  
 Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro  
 165 170 175  
 Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala  
 180 185 190  
 Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val Leu  
 195 200 205  
 Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr Phe  
 210 215 220  
 Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser Asn  
 225 230 235 240  
 Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr  
 245 250 255  
 Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys  
 260 265 270  
 Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro  
 275 280 285  
 Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr  
 290 300

Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu  
 305 310 315 320  
 Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn  
 325 330 335  
 Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp  
 340 345 350  
 Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly  
 355 360 365  
 Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr  
 370 375 380  
 Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser  
 385 390 395 400  
 Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser  
 405 410 415  
 Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser  
 420 425 430  
 Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile  
 435 440 445  
 Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu  
 450 455 460  
 Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His  
 465 470 475 480  
 Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser  
 485 490 495  
 Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly  
 500 505 510  
 Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln  
 515 520 525  
 Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro  
 530 535 540  
 Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu  
 545 550 555 560  
 Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr  
 565 570 575  
 Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg  
 580 585 590

Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu
	595						600					605			
His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu
	610					615					620				
Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr
625					630					635					640
Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val
			645						650					655	
Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg
			660					665					670		
Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn
	675						680					685			
Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser
	690					695					700				
Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro
705					710					715					720
Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr
				725					730					735	
Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr
			740					745					750		
Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu
		755					760					765			
Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys
	770					775					780				
Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro
785					790					795					800
Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala
			805						810					815	
Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu
			820					825					830		
Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	Met	Asn
	835						840					845			
Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys					
	850					855									

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 7..2397

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG CGA GGT CAG	384
Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln	
115 120 125	
AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT ACA AGA ATT	432
Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile	
130 135 140	
ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT GAG GTG AAA	480
Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys	
145 150 155	

AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT CTT GGA CTT	528
Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu	
160 165 170	
GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC	576
Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr	
175 180 185 190	
GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG	624
Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu	
195 200 205	
GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA	672
Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr	
210 215 220	
CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT	720
Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile	
225 230 235	
CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA	768
Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu	
240 245 250	
ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT	816
Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile	
255 260 265 270	
TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA	864
Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys	
275 280 285	
AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT	912
Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala	
290 295 300	
GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA	960
Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly	
305 310 315	
GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA	1008
Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu	
320 325 330	
GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT	1056
Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile	
335 340 345 350	
TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA	1104
Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala Thr	
355 360 365	

TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT	1152
Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser	
370 375 380	
TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC	1200
Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr	
385 390 395	
AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA	1248
Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu	
400 405 410	
ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT	1296
Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser Leu	
415 420 425 430	
GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG	1344
Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys	
435 440 445	
GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT	1392
Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu Asn	
450 455 460	
CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT	1440
Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser Pro	
465 470 475	
GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT	1488
Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser Thr	
480 485 490	
GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA	1536
Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro	
495 500 505 510	
TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA	1584
Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu	
515 520 525	
GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC	1632
Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu His	
530 535 540	
CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG	1680
Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu Gln	
545 550 555	
AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG	1728
Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met Met	
560 565 570	

TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC	1776
Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys Phe	
575 580 585 590	
AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG	1824
Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln Glu	
595 600 605	
ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA	1872
Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile	
610 615 620	
GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG	1920
Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile Leu	
625 630 635	
CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT	1968
Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile	
640 645 650	
CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA	2016
Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly	
655 660 665 670	
GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA	2064
Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu	
675 680 685	
GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA	2112
Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val	
690 695 700	
TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT	2160
Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn	
705 710 715	
CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA	2208
Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly	
720 725 730	
AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT ATT GAA GGA	2256
Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly	
735 740 745 750	
TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG TCC AAA TTT	2304
Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe	
755 760 765	
CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA ATG CAA AAG	2352
Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys	
770 775 780	

CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA GAG AAA	2397
Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys	
785 790 795	
TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG TCTCTCACAG	2457
ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC TTCAGCTCTT	2517
TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC ACTTGAAATG	2577
TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA TTTAAAAAGT	2637
TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT AGTAAGAATG	2697
GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT TCTTTTGTAG	2757
CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT TTAATTTAAC	2817
ATGAACACCC TTAGAAAATG TGTCCATCT ATCTTCCAAA TGCAATTTGA TTGACTGCCC	2877
ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA ATTAGAAAAA	2937
AATTACTAAT TTTACACATT AGATTTTATT TTAATTATTG AATCTGATAT ACTGTGTGCT	2997
TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT AACCATATGA	3057
TACTATCATA CTAAGTAAAC AGATTTTCATA CCTCAGAATG TAAAAGAACT TACTGATTAT	3117
TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT	3161

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala	
1 5 10 15	
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp	
20 25 30	
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu	
35 40 45	
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu	
50 55 60	

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
 65 70 75 80  
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
 85 90 95  
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Ala Val  
 100 105 110  
 Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg  
 115 120 125  
 Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu  
 130 135 140  
 Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val Lys Asn Val  
 145 150 155 160  
 Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly Leu Val Thr  
 165 170 175  
 Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu  
 180 185 190  
 Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His  
 195 200 205  
 Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg  
 210 215 220  
 Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro  
 225 230 235 240  
 His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met  
 245 250 255  
 Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr  
 260 265 270  
 Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val  
 275 280 285  
 Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly  
 290 295 300  
 Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg  
 305 310 315 320  
 Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg  
 325 330 335  
 Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His  
 340 345 350

Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	355	360	365	
Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	370	375	380	
Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	385	390	395	400
Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	405	410	415	
Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	420	425	430	
Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	435	440	445	
Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	450	455	460	
Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	465	470	475	480
Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	485	490	495	
Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	500	505	510	
Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	515	520	525	
Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	530	535	540	
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	545	550	555	560
Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	565	570	575	
Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	580	585	590	
Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	595	600	605	
Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	610	615	620	
Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	625	630	635	640

Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg  
645 650 655

Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn  
660 665 670

Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu  
675 680 685

Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile  
690 695 700

Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met  
705 710 715 720

Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn  
725 730 735

Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp  
740 745 750

Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln  
755 760 765

Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys  
770 775 780

Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
785 790 795

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 7..2613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	

GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATG GTC GCT GTT ATA CCC ATT AAT GGT TCA	576
Thr Gln Pro Ser Ser Ser Met Val Ala Val Ile Pro Ile Asn Gly Ser	
175 180 185 190	
CCT CGA ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA	624
Pro Arg Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys	
195 200 205	
CAA CTA GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT	672
Gln Leu Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His	
210 215 220	
GAA TGT AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA	720
Glu Cys Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile	
225 230 235	

CCT TTT ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG Pro Phe Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu 240 245 250	768
GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys 255 260 265 270	816
GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr 275 280 285	864
GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn 290 295 300	912
CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr 305 310 315	960
GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser 320 325 330	1008
GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val 335 340 345 350	1056
AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile 355 360 365	1104
TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile 370 375 380	1152
GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met 385 390 395	1200
GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe 400 405 410	1248
AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys 415 420 425 430	1296
GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn 435 440 445	1344

CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT	1392
Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu	
450 455 460	
AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA	1440
Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys	
465 470 475	
GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT	1488
Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys	
480 485 490	
GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA	1536
Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu	
495 500 505 510	
TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC	1584
Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His	
515 520 525	
CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT	1632
Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr	
530 535 540	
GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT	1680
Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly	
545 550 555	
TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC	1728
Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr	
560 565 570	
TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG	1776
Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu	
575 580 585 590	
TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT	1824
Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu	
595 600 605	
TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG	1872
Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp	
610 615 620	
ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC	1920
Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp	
625 630 635	
AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA	1968
Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys	
640 645 650	

GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG	2016
Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys	
655 660 665 670	
GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA	2064
Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys	
675 680 685	
GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG	2112
Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met	
690 695 700	
CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT	2160
Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro	
705 710 715	
ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT	2208
Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro	
720 725 730	
AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG	2256
Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu	
735 740 745 750	
AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG	2304
Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met	
755 760 765	
ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT	2352
Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr	
770 775 780	
TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT	2400
Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg	
785 790 795	
GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA	2448
Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys	
800 805 810	
AAA CTA CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA	2496
Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys	
815 820 825 830	
CAT CTC CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT	2544
His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr	
835 840 845	
TCT ACT CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT	2592
Ser Thr Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp	
850 855 860	

ACC TCA AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT 2643  
 Thr Ser Asn Lys Glu Glu Lys  
 865

GTACACCTCT GGATTCATTG TCTCTCACAG ATGTGACTGT ATAACTTTCC CAGGTTCTGT 2703

TTATGGCCAC ATTTAATATC TTCAGCTCTT TTTGTGATA TAAAATGTGC AGATGCAATT 2763

GTTTGGGTGA TTCCTAAGCC ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA 2823

ATCTTGTGTA AATCCTGCCA TTTAAAAAGT TGTAGCAGAT TGTTTCCTCT TCCAAAGTAA 2883

AATTGCTGTG CTTTATGGAT AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG 2943

CCTGTCTGAC TACTTTGCCT TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT 3003

TAATTTATAT GTATATTTTT TTAATTAAAC ATGAACACCC TTAGAAAATG TGTCCTATCT 3063

ATCTTCCAAA TGCAATTGA TTGACTGCCC ATTCACCAA ATTATCCTGA ACTCTTCTGC 3123

AAAAATGGAT ATTATTAGAA ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT 3183

TTACTATTGG AATCTGATAT ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT 3243

AAAAGCTGGA AGCAAAGTAT AACCATATGA TACTATCATA CTA CTACTGAAAC AGATTTTCATA 3303

CCTCAGAATG TAAAAGAACT TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA 3363

GGATTATTGA TAGT 3377

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala  
 1 5 10 15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp  
 20 25 30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu  
 35 40 45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu  
 50 55 60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
 65 70 75 80  
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
 85 90 95  
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu  
 100 105 110  
 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val  
 115 120 125  
 His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
 130 135 140  
 Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala  
 145 150 155 160  
 Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
 165 170 175  
 Pro Ser Ser Ser Met Val Ala Val Ile Pro Ile Asn Gly Ser Pro Arg  
 180 185 190  
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu  
 195 200 205  
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys  
 210 215 220  
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe  
 225 230 235 240  
 Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu  
 245 250 255  
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu  
 260 265 270  
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser  
 275 280 285  
 Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp  
 290 295 300  
 Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met  
 305 310 315 320  
 Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln  
 325 330 335  
 Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro  
 340 345 350

Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	355	360	365	
Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	370	375	380	
Gln	Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	385	390	395	400
Met	Leu	Lys	Ser	Glu	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	405	410	415	
Leu	Leu	Asn	Asp	Asn	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	420	425	430	
Glu	Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	435	440	445	
Ser	Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	450	455	460	
Lys	Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	465	470	475	480
Gly	Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	485	490	495	
Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	500	505	510	
Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	515	520	525	
Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	530	535	540	
Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	545	550	555	560
Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	565	570	575	
Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	580	585	590	
Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	595	600	605	
Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	610	615	620	
Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	625	630	635	640

Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys  
 645 650 655  
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu  
 660 665 670  
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu  
 675 680 685  
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg  
 690 695 700  
 Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu  
 705 710 715 720  
 Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser  
 725 730 735  
 Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser  
 740 745 750  
 Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro  
 755 760 765  
 Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu  
 770 775 780  
 Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu  
 785 790 795 800  
 Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu  
 805 810 815  
 Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu  
 820 825 830  
 Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr  
 835 840 845  
 Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser  
 850 855 860  
 Asn Lys Glu Glu Lys  
 865

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3383 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 7..2619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	
AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	

CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GGG TCG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT	768
Tyr Lys Thr Gly Ser Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu	
240 245 250	
CCA GAG GTT GAA AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA	816
Pro Glu Val Glu Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys	
255 260 265 270	
AAT AAA GAT CTA GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT	864
Asn Lys Asp Leu Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu	
275 280 285	
CAG ACT GAT TCT ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA	912
Gln Thr Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys	
290 295 300	
AGT AAC CTT GAT GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT	960
Ser Asn Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val	
305 310 315	
AGG ACT GTT ATG AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA	1008
Arg Thr Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser	
320 325 330	
GCA AGT GAT CAA CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC	1056
Ala Ser Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys	
335 340 345 350	
ACA GTG AAT CCA AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA	1104
Thr Val Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly	
355 360 365	
TAC ATC TTT AAA GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC	1152
Tyr Ile Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val	
370 375 380	
GAA ATT GGA TCA CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA	1200
Glu Ile Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg	
385 390 395	

GTA ATG GAA TCC ATG CTT AAA TCA GAA GAA GAA CGA TTA TCC ATT CAA	1248
Val Met Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln	
400 405 410	
AAT TTT AGC AAA CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG	1296
Asn Phe Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu	
415 420 425 430	
GCG TGC GCT CTT GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT	1344
Ala Cys Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser	
435 440 445	
CAG AAT CTT GAT TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT	1392
Gln Asn Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn	
450 455 460	
GTG CTT AAT TTA AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT	1440
Val Leu Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe	
465 470 475	
ATC AAA GCA GAA GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA	1488
Ile Lys Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu	
480 485 490	
CGA TGT GAA CAT CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA	1536
Arg Cys Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser	
495 500 505 510	
CCT TTA TTT GAT CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT	1584
Pro Leu Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr	
515 520 525	
GAT CAC CTT GAA TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT	1632
Asp His Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn	
530 535 540	
CAC ACT GCA GCA GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA	1680
His Thr Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys	
545 550 555	
AAA GGT TCA ACT ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA	1728
Lys Gly Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln	
560 565 570	
GCA ACC TCA GCC TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT	1776
Ala Thr Ser Ala Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu	
575 580 585 590	
TCA CTG TTT TAT AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT	1824
Ser Leu Phe Tyr Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn	
595 600 605	

ACA CTT TGT GAA CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC	1872
Thr Leu Cys Glu Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile	
610 615 620	
ATC TGG ACC CTT TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG	1920
Ile Trp Thr Leu Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met	
625 630 635	
AGA GAC AGG CAT TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA	1968
Arg Asp Arg His Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile	
640 645 650	
TGC AAA GTG AAG AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA	2016
Cys Lys Val Lys Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala	
655 660 665 670	
TAC AAG GAT CTT CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG	2064
Tyr Lys Asp Leu Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu	
675 680 685	
ATC AAA GAA GAG GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC	2112
Ile Lys Glu Glu Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val	
690 695 700	
TTC ATG CAG AGA CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG	2160
Phe Met Gln Arg Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg	
705 710 715	
CCC CCT ACC TTG TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG	2208
Pro Pro Thr Leu Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys	
720 725 730	
TTT CCT AGT TCA CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA	2256
Phe Pro Ser Ser Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser	
735 740 745 750	
CCC CTG AAG AGT CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA	2304
Pro Leu Lys Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr	
755 760 765	
AAA ATG ACT CCA AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC	2352
Lys Met Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe	
770 775 780	
GGG ACT TCT GAG AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC	2400
Gly Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser	
785 790 795	
GAC CGT GTG CTC AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA	2448
Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro	
800 805 810	



Met	Pro	Pro	Lys	Thr	Pro	Arg	Lys	Thr	Ala	Ala	Thr	Ala	Ala	Ala	Ala		
1				5					10					15			
Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Glu	Glu	Asp		
			20					25					30				
Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu	Val	Arg	Leu	Glu		
		35					40					45					
Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu	Cys	Gln	Lys	Leu		
	50					55					60						
Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu	Thr	Trp	Glu	Lys		
65					70				75					80			
Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile	Gln	Lys	Lys	Lys		
			85					90						95			
Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Ala	Val	Asp	Leu	Asp	Glu		
			100					105					110				
Met	Ser	Phe	Thr	Phe	Thr	Glu	Leu	Gln	Lys	Asn	Ile	Glu	Ile	Ser	Val		
	115						120					125					
His	Lys	Phe	Phe	Asn	Leu	Leu	Lys	Glu	Ile	Asp	Thr	Ser	Thr	Lys	Val		
	130				135					140							
Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala		
145					150					155				160			
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln		
			165					170					175				
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys		
			180					185					190				
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met		
	195					200						205					
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp		
	210					215					220						
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys		
225					230				235					240			
Thr	Gly	Ser	Asn	Ser	Leu	Gly	Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu		
			245					250					255				
Val	Glu	Asn	Leu	Ser	Lys	Arg	Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys		
		260						265					270				
Asp	Leu	Asp	Ala	Arg	Leu	Phe	Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr		
	275						280					285					

Asp Ser Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn  
 290 295 300

Leu Asp Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr  
 305 310 315 320

Val Met Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser  
 325 330 335

Asp Gln Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val  
 340 345 350

Asn Pro Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile  
 355 360 365

Phe Lys Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile  
 370 375 380

Gly Ser Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met  
 385 390 395 400

Glu Ser Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe  
 405 410 415

Ser Lys Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys  
 420 425 430

Ala Leu Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn  
 435 440 445

Leu Asp Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu  
 450 455 460

Asn Leu Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys  
 465 470 475 480

Ala Glu Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys  
 485 490 495

Glu His Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu  
 500 505 510

Phe Asp Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His  
 515 520 525

Leu Glu Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr  
 530 535 540

Ala Ala Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly  
 545 550 555 560

Ser Thr Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr  
 565 570 575

Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	580	585	590	
Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	595	600	605	
Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	610	615	620	
Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	625	630	635	640
Arg	His	Leu	Asp	Gln	Ile	Met	Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	645	650	655	
Val	Lys	Asn	Ile	Asp	Leu	Lys	Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	660	665	670	
Asp	Leu	Pro	His	Ala	Val	Gln	Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	675	680	685	
Glu	Glu	Glu	Tyr	Asp	Ser	Ile	Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	690	695	700	
Gln	Arg	Leu	Lys	Thr	Asn	Ile	Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	705	710	715	720
Thr	Leu	Ser	Pro	Ile	Pro	His	Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	725	730	735	
Ser	Ser	Pro	Leu	Arg	Ile	Pro	Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	740	745	750	
Lys	Ser	Pro	Tyr	Lys	Ile	Ser	Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	755	760	765	
Thr	Pro	Arg	Ser	Arg	Ile	Leu	Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	770	775	780	
Ser	Glu	Lys	Phe	Gln	Lys	Ile	Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	785	790	795	800
Val	Leu	Lys	Arg	Ser	Ala	Glu	Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	805	810	815	
Lys	Leu	Arg	Phe	Asp	Ile	Glu	Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	820	825	830	
His	Leu	Pro	Gly	Glu	Ser	Lys	Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	835	840	845	
Ser	Thr	Arg	Thr	Arg	Met	Gln	Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	850	855	860	

Thr Ser Asn Lys Glu Glu Lys  
865 870

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..2790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC ACC GCC GCC	48
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala	
1 5 10	
GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC CCT CCT GAG	96
Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu	
15 20 25 30	
GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT CTC GTC AGG	144
Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg	
35 40 45	
CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA TTA TGT CAG	192
Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln	
50 55 60	
AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG TTA ACT TGG	240
Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp	
65 70 75	
GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT ATT CAA AAG	288
Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys	
80 85 90	
AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA GTT GAC CTA	336
Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu	
95 100 105 110	
GGT GAT ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC ATA GAA ATC	384
Gly Asp Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile	
115 120 125	
AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT ACC AGT ACC	432
Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr	
130 135 140	

AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT GAT GTA TTG	480
Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu	
145 150 155	
TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT ATA TAT TTG	528
Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu	
160 165 170	
ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT GCA TTG GTG	576
Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val	
175 180 185 190	
CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG GAA GTA TTA	624
Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu	
195 200 205	
CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG CTA TGT GTC	672
Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val	
210 215 220	
CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC AAA GAA CCA	720
Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro	
225 230 235	
TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA ACA CCC AGG	768
Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg	
240 245 250	
CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA GAA AAT GAT	816
Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp	
255 260 265 270	
ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT AAT ATA GAT	864
Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp	
275 280 285	
GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT ATG AAT TCT	912
Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser	
290 295 300	
CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA AAT CTT TCT	960
Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser	
305 310 315	
AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA GAT GCA AGA	1008
Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg	
320 325 330	
TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT ATA GAC AGT	1056
Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser	
335 340 345 350	

TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT GAA GAG GTG	1104
Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val	
355 360 365	
AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG AAC ACT ATC	1152
Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile	
370 375 380	
CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA CCT TCA GAA	1200
Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu	
385 390 395	
AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA AAA GAA AGT	1248
Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser	
400 405 410	
ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA GAG AAA TTT	1296
Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe	
415 420 425 430	
GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA CAG CGA TAC	1344
Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr	
435 440 445	
AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC ATG CTT AAA	1392
Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys	
450 455 460	
TCA GAA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA CTT CTG AAT	1440
Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn	
465 470 475	
GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT GAG GTT GTA	1488
Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val	
480 485 490	
ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT TCT GGA ACA	1536
Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr	
495 500 505 510	
GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA AAA GCC TTT	1584
Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe	
515 520 525	
GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA GGC AAC TTG	1632
Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu	
530 535 540	
ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT CGA ATC ATG	1680
Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met	
545 550 555	

GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT CTT ATT AAA	1728
Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys	
560 565 570	
CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA TCT GCT TGT	1776
Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys	
575 580 585 590	
CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA GAT ATG TAT	1824
Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr	
595 600 605	
CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT ACG CGT GTA	1872
Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val	
610 615 620	
AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC TTC CAG ACC	1920
Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr	
625 630 635	
CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT AAA AAA GTG	1968
Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val	
640 645 650	
TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA CGC CTT CTG	2016
Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu	
655 660 665 670	
TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT TTC CAG CAC	2064
Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His	
675 680 685	
ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT TTG GAC CAA	2112
Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln	
690 695 700	
ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG AAT ATA GAC	2160
Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp	
705 710 715	
CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT CCT CAT GCT	2208
Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala	
720 725 730	
GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG GAG TAT GAT	2256
Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp	
735 740 745 750	
TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA CTG AAA ACA	2304
Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr	
755 760 765	

AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG TCA CCA ATA	2352
Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile	
770 775 780	
CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA CCC TTA CGG	2400
Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg	
785 790 795	
ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT CCA TAT AAA	2448
Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys	
800 805 810	
ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA AGA TCA AGA	2496
Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg	
815 820 825 830	
ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG AAG TTC CAG	2544
Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln	
835 840 845	
AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC AAA AGA AGT	2592
Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser	
850 855 860	
GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA CGC TTT GAT	2640
Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp	
865 870 875	
ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC CCA GGA GAG	2688
Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu	
880 885 890	
TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT CGA ACA CGA	2736
Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg	
895 900 905 910	
ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA AAC AAG GAA	2784
Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu	
915 920 925	
GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT GGATTCATTG	2840
Glu Lys	
TCTCTCACAG ATGTGACTGT ATAACCTTCC CAGGTTCTGT TTATGGCCAC ATTTAATATC	2900
TTCAGCTCTT TTTGTGGATA TAAAATGTGC AGATGCAATT GTTTGGGTGA TTCCTAAGCC	2960
ACTTGAAATG TTAGTCATTG TTATTTATAC AAGATTGAAA ATCTTGTGTA AATCCTGCCA	3020
TTTAAAAAGT TGTAGCAGAT TGTTCCTCT TCCAAAGTAA AATTGCTGTG CTTTATGGAT	3080
AGTAAGAATG GCCCTAGAGT GGGAGTCCTG ATAACCCAGG CCTGTCTGAC TACTTTGCCT	3140

TCTTTTGTAG CATATAGGTG ATGTTTGCTC TTGTTTTTAT TAATTTATAT GTATATTTTT 3200  
 TTAATTTAAC ATGAACACCC TTAGAAAATG TGTCTTATCT ATCTTCCAAA TGCAATTTGA 3260  
 TTGACTGCCC ATTCACCAAA ATTATCCTGA ACTCTTCTGC AAAAATGGAT ATTATTAGAA 3320  
 ATTAGAAAAA AATTACTAAT TTTACACATT AGATTTTATT TTACTATTGG AATCTGATAT 3380  
 ACTGTGTGCT TGTTTTATAA AATTTTGCTT TTAATTAAAT AAAAGCTGGA AGCAAAGTAT 3440  
 AACCATATGA TACTATCATA CTACTGAAAC AGATTTTATA CCTCAGAATG TAAAAGAACT 3500  
 TACTGATTAT TTTCTTCATC CAACTTATGT TTTTAAATGA GGATTATTGA TAGT 3554

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala  
 1 5 10 15  
 Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp  
 20 25 30  
 Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu  
 35 40 45  
 Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu  
 50 55 60  
 Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys  
 65 70 75 80  
 Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys  
 85 90 95  
 Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Gly Asp  
 100 105 110  
 Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val  
 115 120 125  
 His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val  
 130 135 140

Asp	Asn	Ala	Met	Ser	Arg	Leu	Leu	Lys	Lys	Tyr	Asp	Val	Leu	Phe	Ala	145	150	155	160
Leu	Phe	Ser	Lys	Leu	Glu	Arg	Thr	Cys	Glu	Leu	Ile	Tyr	Leu	Thr	Gln	165	170	175	
Pro	Ser	Ser	Ser	Ile	Ser	Thr	Glu	Ile	Asn	Ser	Ala	Leu	Val	Leu	Lys	180	185	190	
Val	Ser	Trp	Ile	Thr	Phe	Leu	Leu	Ala	Lys	Gly	Glu	Val	Leu	Gln	Met	195	200	205	
Glu	Asp	Asp	Leu	Val	Ile	Ser	Phe	Gln	Leu	Met	Leu	Cys	Val	Leu	Asp	210	215	220	
Tyr	Phe	Ile	Lys	Leu	Ser	Pro	Pro	Met	Leu	Leu	Lys	Glu	Pro	Tyr	Lys	225	230	235	240
Thr	Ala	Val	Ile	Pro	Ile	Asn	Gly	Ser	Pro	Arg	Thr	Pro	Arg	Arg	Gly	245	250	255	
Gln	Asn	Arg	Ser	Ala	Arg	Ile	Ala	Lys	Gln	Leu	Glu	Asn	Asp	Thr	Arg	260	265	270	
Ile	Ile	Glu	Val	Leu	Cys	Lys	Glu	His	Glu	Cys	Asn	Ile	Asp	Glu	Val	275	280	285	
Lys	Asn	Val	Tyr	Phe	Lys	Asn	Phe	Ile	Pro	Phe	Met	Asn	Ser	Leu	Gly	290	295	300	
Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315	320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395	400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430	

Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475	480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	530	535	540	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	545	550	555	560
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	565	570	575	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	580	585	590	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	595	600	605	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	610	615	620	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	625	630	635	640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	645	650	655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	660	665	670	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	675	680	685	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	690	695	700	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	705	710	715	720

Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	725	730	735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	740	745	750	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	755	760	765	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	770	775	780	
Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro	785	790	795	800
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser	805	810	815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu	820	825	830	
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile	835	840	845	
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu	850	855	860	
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu	865	870	875	880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys	885	890	895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln	900	905	910	
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys	915	920	925	